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RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/910,059

TIME: 15:18:02

Input Set : A:\pto_vsk.txt

Output Set: N:\CRF3\10292001\I910059.raw

3 <110> APPLICANT: Copley, Clive G
 4 Edge, Michael Derek
 5 Emery, Stephen Charles
 7 <120> TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
 Antibody, and
 8 Their Therapeutic use in an Adept System
 10 <130> FILE REFERENCE: 1991-209
 12 <140> CURRENT APPLICATION NUMBER: US 09/910,059
 13 <141> CURRENT FILING DATE: 2001-07-23
 15 <150> PRIOR APPLICATION NUMBER: US 09/171,945
 16 <151> PRIOR FILING DATE: 1998-10-29
 18 <150> PRIOR APPLICATION NUMBER: PCT/GB97/01165
 19 <151> PRIOR FILING DATE: 1997-04-29
 21 <150> PRIOR APPLICATION NUMBER: GB 9703103.3
 22 <151> PRIOR FILING DATE: 1997-02-14
 24 <150> PRIOR APPLICATION NUMBER: GB9609405.7
 25 <151> PRIOR FILING DATE: 1996-05-04
 27 <160> NUMBER OF SEQ ID NOS: 131
 29 <170> SOFTWARE: PatentIn version 3.1
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 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: light chain cDNA foward primer
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 44 <211> LENGTH: 31
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 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
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 51 <400> SEQUENCE: 2
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 56 <211> LENGTH: 34
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Mus musculus
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 63 1 5 10 15
 66 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
 67 20 25 30
 70 Tyr Met
 74 <210> SEQ ID NO: 4
 75 <211> LENGTH: 24
 76 <212> TYPE: DNA

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77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: light chain cDNA backward primer ✓
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89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: light chain cDNA backward primer ✓
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99 <211> LENGTH: 22
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence ✓
103 <220> FEATURE:
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112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence ✓
115 <220> FEATURE:
116 <223> OTHER INFORMATION: heavy chain cDNA backward primer
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123 <211> LENGTH: 357
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130 ataacctgca gtgccagctc aagtgttaact tacatgcact gggtccagca gaagccaggc 120
132 acttctccca aactctggat ttatagcaca tccaacctgg cttctggagt ccctgctcgc 180
134 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
136 gatgctgcca cttattactg ccagcaaaagg agtacttacc cgctcacgtt cgggtgctggg 300
138 accaagctgg agctgaaaacg ggctgatgct gcaccaactg tatccatctt caagctt 357
141 <210> SEQ ID NO: 9
142 <211> LENGTH: 108
143 <212> TYPE: PRT
144 <213> ORGANISM: Mus musculus
146 <400> SEQUENCE: 9
148 Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
149 1 5 10 15
152 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
153 20 25 30

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156 His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
157      35      40      45
160 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
161      50      55      60
164 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
165 65      70      75      80
168 Asp Ala Ala Thr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
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172 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
173      100      105
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177 <211> LENGTH: 360
178 <212> TYPE: DNA
179 <213> ORGANISM: Mus musculus
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184 tcctgcacag cttctggctt caacattaaa gacaactata tgcactgggt gaagcagagg      120
186 cctgaacagg gcctggagtg gattgcatgg attgatcctg agaatgggtga tactgaatat      180
188 gccccgaagt tccggggcaa ggccactttg actgcagact catcctccaa cacagcctac      240
190 ctgcacctca gcagcctgac atctgaggac actgccgtct attactgtca tgtcctgac      300
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196 <211> LENGTH: 120
197 <212> TYPE: PRT
198 <213> ORGANISM: Mus musculus
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203 1      5      10      15
206 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
207      20      25      30
210 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
211      35      40      45
214 Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
215      50      55      60
218 Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr
219 65      70      75      80
222 Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
223      85      90      95
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230 Gly Thr Ser Val Ala Val Ser Ser
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235 <211> LENGTH: 39
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237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: light chain primer
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243 aagctttccc gcggggacat tgagctcacc cagtctcca 39
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248 <212> TYPE: DNA
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251 <220> FEATURE:
252 <223> OTHER INFORMATION: light chain primer ✓
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255 aagctttctcg agcttgggtcc cagcaccgaa 30
258 <210> SEQ ID NO: 14
259 <211> LENGTH: 36
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence ✓
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264 <223> OTHER INFORMATION: heavy chain primer ✓
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283 <211> LENGTH: 705
284 <212> TYPE: DNA
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287 <220> FEATURE:
288 <223> OTHER INFORMATION: chimaeric light chain sequence ✓
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291 atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
293 cgcgggggaca ttgagctcac ccagtctcca gcaatcatgt ctgcatctcc agggggagaag 120
295 gtcaccataa cctgcagtgc cagctcaagt gtaacttaca tgcaactggt ccagcagaag 180
297 ccaggcactt ctcccaaact ctggatttat agcacatcca acctggcttc tggagtccct 240
299 gctcgcttca gtggcagtgg atctgggacc tcttactctc tcacaatcag ccgaatggag 300
301 gctgaagatg ctgccactta ttactgccag caaaggagta cttacccgct cacgttcggt 360
303 gctgggacca agctcgagat caaacggact gtggctgcac catctgtctt catcttcccg 420
305 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
307 tatcccagag aggccaaaagt acagtggaa gtggataacg ccctccaatc gggtaaactcc 540
309 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600
311 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 660
313 ggcttgagtt cgcccgtcac aaagagcttc aacaggggag agtgt 705
316 <210> SEQ ID NO: 17
317 <211> LENGTH: 235
318 <212> TYPE: PRT
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:

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322 <223> OTHER INFORMATION: chimaeric light chain sequence

324 <400> SEQUENCE: 17

326 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

327 1 5 10 15

330 Val Ile Met Ser Arg Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile

331 20 25 30

334 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

335 35 40 45

338 Ser Ser Val Thr Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser

339 50 55 60

342 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro

343 65 70 75 80

346 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile

347 85 90 95

350 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg

351 100 105 110

354 Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys

355 115 120 125

358 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

359 130 135 140

362 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

363 145 150 155 160

366 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln

367 165 170 175

370 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

371 180 185 190

374 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

375 195 200 205

378 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

379 210 215 220

382 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

383 225 230 235

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387 <211> LENGTH: 765

388 <212> TYPE: DNA

389 <213> ORGANISM: Artificial Sequence

391 <220> FEATURE:

392 <223> OTHER INFORMATION: chimaeric HuIgG2 Fd construct

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397 gtgcagctgc agcartcagg ggcagagctt gtgaggtcag gggcctcagt caagttgtcc 120

399 tgcacagctt ctggcttcaa cattaaagac aactatatgc actgggtgaa gcagaggcct 180

401 gaacagggcc tggagtggat tgcattgatt gatcctgaga atggtgatac tgaatatgcc 240

403 ccgaagtcc ggggcaaggc cactttgact gcagactcat cctccaacac agcctacctg 300

405 cacctcagca gcctgacatc tgaggacact gccgtctatt actgtcatgt cctgatctat 360

407 gctggttatt tggctatgga ctactggggt caaggaacct cagtcgccgt gagctcggct 420

409 agcaccaagg gaccatcggt ctccccctg gccccctgct ccaggagcac ctccgagagc 480

411 acagccgccc tgggtgcct ggtcaaggac tacttcccgc aaccggtgac ggtgtcgtgg 540

413 aactcaggcg ctctgaccag cggcgtgcac accttcccgc ctgtcctaca gtcctcagga 600

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/910,059

DATE: 10/29/2001

TIME: 15:18:03

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